L Number	Hits	Search Text	DB	Time stamp
1	2	6140446.pn.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/02/04 15:01
5	4	6242568.pn. or 6140466.pn.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/02/04 15:04
6	160	barbas-$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/02/04 15:05
7	63	gottesfeld-$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/02/04 15:05
8	814	wright-p$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/02/04 15:06
9	7	barbas-$.in. and gottesfeld-$.in. and wright-p$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/02/04 15:06
10	1023	barbas-$.in. or gottesfeld-$.in. or wright-p$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/02/04 15:06
11	29	(barbas-$.in. or gottesfeld-$.in. or wright-p$.in.) and (zinc adj2 finger)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/02/04 15:06
12	22	((barbas-$.in. or gottesfeld-$.in. or wright-p$.in.) and (zinc adj2 finger)) not (barbas-$.in. and gottesfeld-$.in. and wright-p$.in.)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/02/04 15:06
13	3653	zinc adj2 finger	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/02/04 15:06
14	478	(zinc adj2 finger).ti.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/02/04 15:06
15	17	((zinc adj2 finger) with bind$4 with (new or different)).ti.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/02/04 15:06
16	338	ladner-$.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/02/04 15:07
17	14	ladner-$.in. and (zinc adj2 finger)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/02/04 15:07
18	155	(zinc adj2 finger) with librar$4	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/02/04 15:07

19	99	(zinc adj2 finger) with librar$4 with (produc$6 or screen$4 or construct$4 or design$4)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/02/04 15:07
20	22	((zinc adj2 finger) with librar$4 with (produc$6 or screen$4 or construct$4 or design$4)) with method	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/02/04 15:07
21	18	(((zinc adj2 finger) with librar$4 with (produc$6 or screen$4 or construct$4 or design$4)) with method) not (barbas-$.in. or gottesfeld-$.in. or wright-p$.in.)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/02/04 15:07
22	2	((zinc adj2 finger) with librar$4 with (produc$6 or screen$4 or construct$4 or design$4)).ti.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/02/04 15:08
23	5	((zinc adj2 finger) with librar$4 with (produc$6 or screen$4 or construct$4 or design$4)).clm.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/02/04 15:08

-continued

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GCGTGGGCGG CGTGGGCG 18

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GCGTGGGCGG GGGCGGGG 18

What is claimed is:

1. An isolated zinc finger-nucleotide binding polypeptide variant comprising at least three zinc finger modules that bind to a target cellular nucleotide sequence and modulate the transcriptional function of the cellular nucleotide sequence, wherein the amino acid sequence of each zinc finger module that binds a target cellular nucleotide comprises two cysteines and two histidines whereby both cysteines are amino proximal to both histidines and wherein each of three modules of said variant has at least one amino acid sequence modification.

2. The variant of claim 1, wherein the modulation is enhancement of transcription of a gene operatively linked to the cellular nucleotide sequence.

3. The variant of claim 1, wherein the modulation is suppression of transcription of a gene operatively linked to the cellular nucleotide sequence.

4. The variant of claim 1, which is derived from a zinc finger-nucleotide binding polypeptide selected from the group consisting of zif268 and TFIIIA.

5. The variant of claim 1, wherein the cellular nucleotide sequence is DNA.

6. The variant of claim 1, wherein the cellular nucleotide sequence is RNA.

7. The variant of claim 1, wherein the polypeptide contains a linker region between zinc fingers, the linker comprising the amino acid sequence TGEKP.

8. The variant of claim 1, wherein the cellular nucleotide sequence is a structural gene nucleotide sequence.

9. The variant of claim 1, wherein the cellular nucleotide sequence is a promoter nucleotide sequence.

10. The variant of claim 9, wherein the promoter is an onco-promoter.

11. The variant of claim 10, wherein the promoter is a viral promoter.

12. The variant of claim 1, wherein the cellular nucleotide sequence is a retroviral nucleotide sequence.

13. The variant of claim 12, wherein the retrovirus is a human T-cell lymphotrophic virus (HTLV).

14. The variant of claim 13, wherein the retrovirus is HTLV-1 or HTLV-2.

15. The variant of claim 12, wherein the retrovirus is a human immunodeficiency virus (HIV).

16. The variant of claim 15, wherein the retrovirus is HIV-1 or HIV-2.

17. The variant of claim 1, wherein the cellular nucleotide sequence is an oncogene nucleotide sequence.

18. The variant of claim 1, wherein the cellular nucleotide sequence is a plant cellular nucleotide sequence.

19. The isolated zinc finger-nucleotide binding polypeptide variant of claim 1, comprising at least four zinc finger modules that bind to a cellular nucleotide sequence and modulate the transcriptional function of the cellular nucleotide sequence.

20. The isolated zinc finger-nucleotide binding polypeptide variant of claim 1, comprising at least six zinc finger modules that bind to a cellular nucleotide sequence and modulate the transcriptional function of the cellular nucleotide sequence.

21. The isolated zinc finger-nucleotide binding polypeptide variant of claim 1, wherein the polypeptide binds to a cellular nucleotide sequence having 18 contiguous base pairs.

22. The isolated zinc finger-nucleotide binding polypeptide variant of claim 1, wherein the polypeptide binds to a cellular nucleotide sequence comprising two 9-base pair binding sites.

23. An isolated zinc finger-nucleotide binding polypeptide variant having at least six zinc finger modules that bind to a target cellular nucleotide sequence and modulate the transcriptional function of the cellular nucleotide sequence, wherein each zinc finger module that binds a target cellular nucleotide sequence is modified, wherein the polypeptide binds to a cellular nucleotide sequence comprising two 9-base pair binding sites and wherein the two 9-base pair binding sites are separated by a variable number of nucleotides.

24. The isolated zinc finger-nucleotide binding polypeptide variant of claim 23, wherein the two 9-base pair binding sites are contiguous.

25. A n isolated nucleotide sequence encoding a zinc finger-nucleotide binding polypeptide variant of claim 1.

26. The nucleotide sequence of claim 19, further comprising a transcriptional activation domain in operable linkage with the nucleotide sequence.

27. The nucleotide sequence of claim 19, further comprising a repressor domain in operable linkage with the nucleotide sequence.

28. A nucleotide sequence encoding a zinc finger nucleotide binding polypeptide variant having the zinc finger

modules that bind to a target cellular nucleotide sequence and modulate the transcriptional function of the cellular nucleotide sequence, wherein each zinc finger module that binds a target cellular nucleotide sequence is modified comprising a transcriptional activation domain in operable linkage with the nucleotide sequence, wherein the transcriptional activational domain is a herpes simplex virus VP16 protein.

29. A nucleotide sequence encoding a zinc finger-nucleotide binding polypeptide variant having zinc finger modules that bind to a target cellular nucleotide sequence and modulate the transcriptional function of the cellular nucleotide sequence, wherein each zinc finger module that binds a target cellular nucleotide sequence is modified comprising a repressor domain in operable linkage with the nucleotide sequence, wherein the repressor domain is the Kruppel-associated box A domain (KRAB-A).

30. A recombinant expression vector containing a nucleotide sequence of claim **19**.

31. An in vitro method for inhibiting a transcriptional function of a target cellular nucleotide sequence comprising a zinc finger-nucleotide binding motif, the method comprising contacting the motif with an effective amount of a zinc finger-nucleotide binding polypeptide variant comprised of at least three zinc finger molecules, wherein the amino acid sequence of each zinc finger module that binds the motif comprises two cysteines and two histidines whereby both cysteines are amino proximal to both histidines and wherein each of three modules has at least one amino acid sequence modification, thereby inhibiting a transcriptional function of the sequence.

32. The method of claim **26**, wherein the zinc finger binding polypeptide variant is a truncated zinc finger protein.

33. The method of claim **31**, wherein the cellular nucleotide sequence is DNA.

34. The method of claim **31**, wherein the cellular nucleotide sequence is RNA.

35. The method of claim **31**, wherein the cellular nucleotide sequence is a structural gene nucleotide sequence.

36. The method of claim **31**, wherein the cellular nucleotide sequence is a promoter nucleotide sequence.

37. The method of claim **31**, wherein the cellular nucleotide sequence is an oncogene nucleotide sequence.

38. The method of claim **31**, wherein the cellular nucleotide sequence is a plant cellular nucleotide sequence.

39. The method of claim **26**, wherein the variant is derived from a zinc finger-nucleotide binding polypeptide selected from the group consisting of Zif268 and TFIIIA.

40. A method for isolating a zinc finger-nucleotide binding polypeptide variant which binds to a cellular nucleotide sequence comprising:

a) identifying the amino acids in a zinc finger-nucleotide binding polypeptide that bind to a first cellular nucleotide sequence and modulate the function of a nucleotide sequence;

b) creating an expression library encoding the polypeptide variant containing randomized substitution of the amino acids identified in step a) above;

c) expressing the library in a suitable host cell; and

d) isolating a clone that produces a polypeptide variant that binds to a second cellular nucleotide sequence and modulates the function of the second nucleotide sequence;

wherein the variant is comprised of at least three zinc finger modules and wherein the amino acid sequence of each module that binds the second nucleotide sequence comprises two cysteines and two histidines whereby both cysteines are amino proximal to both histidines and wherein each of three modules of said variant has at least one amino acid sequence modification.

41. The method of claim **40**, wherein the library is expressed in a phage surface expression system.

42. The method of claim **41**, wherein the phage expression system includes a reducing reagent which allows folding of expression products on the phage surface.

43. The method of claim **42**, wherein the reducing reagent is dithiothreitol.

44. The method of claim **40**, wherein the library is randomized by PCR using primers containing degenerate triplet codons at sequence locations corresponding to the determined amino acids.

45. The method of claim **40**, wherein the variant is derived from a zinc finger-nucleotide binding polypeptide selected from the group consisting of zif268 and TFIIIA.

46. The method of claim **45**, wherein the variant derived from the zinc finger-nucleotide binding polypeptide zif268 is modified at any of residues 1, 3, 4, 5, 6 or 7 as set forth in SEQ ID NO:14.

47. The method of claim **45**, wherein the variant derived from the zinc finger-nucleotide binding polypeptide zif268 is modified at any of residues 1, 2, 3, 4, 5 or 6 as set forth in SEQ ID NO:15.

48. The method of claim **45**, wherein the variant derived from the zinc finger-nucleotide binding polypeptide zif268 is modified at any of residues 1, 3, 4, 5, 6 or 7 as set forth in SEQ ID NO:5.

49. The method of claim **40**, wherein the modulation of function is enhancement of transcription of a gene operatively linked to the cellular nucleotide sequence.

50. The method of claim **40**, wherein the modulation of function is suppression of transcription of a gene operatively linked to the cellular nucleotide sequence.

51. The method of claim **40**, wherein the cellular nucleotide sequence is DNA.

52. The method of claim **40**, wherein the cellular nucleotide sequence is RNA.

53. A zinc finger-nucleotide binding polypeptide variant produced by the method of claim **40**.

54. A method for identifying a zinc finger-nucleotide binding polypeptide variant comprised of at least three zinc finger modules, which modulates the transcriptional function of cellular nucleotide sequence and binds to a zinc finger-nucleotide binding motif, wherein the amino acid sequence of each module that binds to a zinc finger nucleotide binding motif comprises two cysteines and two histidines whereby both cysteines are amino proximal to both histidines and wherein each of three modules of said variant has at least one amino acid sequence modification, said method comprising:

a) incubating the components comprising a nucleotide sequence encoding the putative modulating variant operably linked to a first inducible promoter, and a reporter gene operably linked to a second inducible promoter and a zinc finger-nucleotide binding motif, wherein the incubating is carried out under conditions sufficient to allow the components to interact; and

b) measuring the effect of the putative modulating variant on the expression of the reporter gene.

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```
Arg Asn Phe Ser Arg Ser Asp His Leu Thr Thr His Ile Arg Thr His
    130                 135                 140

ACA GGC GAG AAG CCT TTT GCC TGT GAC ATT TGT GGG AGG AAG TTT GCC      480
Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala
145                 150                 155                 160

AGG AGT GAT GAA CGC AAG AGG CAT ACC AAA ATC CAT TTA AGA CAG AAG      528
Arg Ser Asp Glu Arg Lys Arg His Thr Lys Ile His Leu Arg Gln Lys
                165                 170                 175

GAC TCT AGA ACT AGT                                                  543
Asp Ser Arg Thr Ser
            180
```

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 181 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```
Met Leu Glu Leu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg
  1               5                  10                  15

Phe Ser Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly
             20                  25                  30

Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser
         35                  40                  45

Asp His Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe
     50                  55                  60

Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys
 65                  70                  75                  80

Arg His Thr Lys Ile His Thr Gly Glu Lys Pro Tyr Ala Cys Pro Val
                 85                  90                  95

Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp Glu Leu Thr Arg His
            100                 105                 110

Ile Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Cys Met
        115                 120                 125

Arg Asn Phe Ser Arg Ser Asp His Leu Thr Thr His Ile Arg Thr His
    130                 135                 140

Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala
145                 150                 155                 160

Arg Ser Asp Glu Arg Lys Arg His Thr Lys Ile His Leu Arg Gln Lys
                165                 170                 175

Asp Ser Arg Thr Ser
            180
```

What is claimed is:

1. A method for isolating a zinc finger-nucleotide binding polypeptide variant which binds to a cellular nucleotide sequence comprising:

a) identifying the amino acids in a zinc finger-nucleotide binding polypeptide that bind to a first cellular nucleotide sequence and modulate the function of a nucleotide sequence;

b) creating an expression library encoding the polypeptide variant containing randomized substitution of the amino acids identified in step a) above;

c) expressing the library in a suitable host cell; and

d) isolating a clone that produces a polypeptide variant that binds to a second cellular nucleotide sequence and modulates the function of the second nucleotide sequence;

wherein the variant is comprised of at least two zinc finger modules and wherein the amino acid sequence of each module that binds the second nucleotide sequence comprises two cysteines and two histidines whereby both cysteines are amino proximal to both histidines and wherein each of two modules of said variant has at least one amino acid sequence modification.

2. The method of claim 1, wherein the library is expressed in a phage surface expression system.

3. The method of claim 1, wherein the phage expression system includes a reducing reagent which allows folding of expression products on the phage surface.

4. The method of claim 3, wherein the reducing reagent is dithiothreitol.

5. The method of claim 1, wherein the library is randomized by PCR using primers containing degenerate triplet codons at sequence locations corresponding to the determined amino acids.

6. The method of claim 1, wherein the modulation of function is enhancement of transcription of a gene operatively linked to the cellular nucleotide sequence.

7. The method of claim 1, wherein the modulation of function is suppression of transcription of a gene operatively linked to the cellular nucleotide sequence.

8. The method of claim 1, wherein the cellular nucleotide sequence is DNA.

9. The method of claim 1, wherein the cellular nucleotide sequence is RNA.

10. The method of claim 1, wherein the variant is derived from a zinc finger-nucleotide binding polypeptide selected from the group consisting of zif 268 and TFIIIA.

11. The method of claim 1, wherein the variant derived from the zinc finger-nucleotide binding polypeptide zif268 is modified at any of residues 1, 3, 4, 5, 6 or 7 as set forth in SEQ ID NO:14.

12. The method of claim 1, wherein the variant derived from the zinc finger-nucleotide binding polypeptide zif268 is modified at any of residues 1, 2, 3, 4, 5 or 6 as set forth in SEQ ID NO:15.

13. The method of claim 1, wherein the variant derived from the zinc finger-nucleotide binding polypeptide zif268 is modified at any of residues 1, 3, 4, 5, 6 or 7 as set forth in SEQ ID NO:5.

14. A method for identifying a zinc finger-nucleotide binding polypeptide variant comprised of at least two zinc finger modules, which modulates the transcriptional function of cellular nucleotide sequence and binds to a zinc finger-nucleotide binding motif, wherein the amino acid sequence of each module that binds to a zinc finger nucleotide binding motif comprises two cysteines and two histidines whereby both cysteines are amino proximal to both histidines and wherein each of two modules of said variant has at least one amino acid sequence modification, said method comprising:

a) incubating the components comprising a nucleotide sequence encoding the putative modulating variant operably linked to a first inducible promoter, and a reporter gene operably linked to a second inducible promoter and a zinc finger-nucleotide binding motif, wherein the incubating is carried out under conditions sufficient to allow the components to interact; and

b) measuring the effect of the putative modulating variant on the expression of the reporter gene.

15. The method of claim 14, wherein the modulation is inhibition of gene expression.

16. The method of claim 14, wherein the modulation is enhancement of gene expression.

17. The method of claim 14, wherein the first inducible promoter is the arabinase promoter.

18. The method of claim 14, wherein the second inducible promoter is the lactose promoter.

19. The method of claim 14, wherein the incubating is performed in vitro.

20. The method of claim 14, wherein the incubating is performed in vivo.

21. The method of claim 14, wherein the reporter gene is β-galactosidase.

22. A method of modulating transcription of a cellular nucleotide sequence associated with a zinc finger-nucleotide binding motif, comprising contacting the zinc finger-nucleotide in cells in vitro with an effective amount of a zinc finger-nucleotide binding polypeptide variant comprised of at least two zinc finger modules that binds to the zinc finger-nucleotide binding motif, wherein the amino acid sequence of each module that binds the motif comprises two cysteines and two histidines whereby both cysteines are amino proximal to both histidines and wherein each of two modules of said variant has at least one amino acid sequence modification, thereby modulating transcriptional activity of the cellular nucleotide sequence.

23. The method of claim 22, wherein an expression vector comprising a polynucleotide sequence encoding a zinc finger-nucleotide binding polypeptide variant is introduced into the cells.

24. The method of claim 23, wherein the expression vector is a virus.

25. The method of claim 22, wherein the modulation is enhancement of transcription of a gene operatively linked to the cellular nucleotide sequence.

26. The method of claim 22, wherein the modulation is suppression of transcription of a gene operatively linked to the cellular nucleotide sequence.

27. The method of claims 1, 14, or 22 wherein the variant is derived from a zinc finger-nucleotide binding polypeptide selected from the group consisting of zif268 and TFIIIA.

28. An isolated zinc finger-nucleotide binding polypeptide variant comprising at least two zinc finger modules that bind to a target cellular nucleotide sequence and modulate the transcriptional function of the cellular nucleotide sequence, wherein the amino acid sequence of each zinc finger module that binds a target cellular nucleotide comprises two cysteines and two histidines whereby both cysteines are amino proximal to both histidines and wherein each of two modules of said variant has at least one amino acid sequence modification.

29. The variant of claim 28, wherein the modulation is enhancement of transcription of a gene operatively linked to the cellular nucleotide sequence.

30. The variant of claim 28, wherein the modulation is suppression of transcription of a gene operatively linked to the cellular nucleotide sequence.

31. The variant of claim 28, which is derived from a zinc finger-nucleotide binding polypeptide selected from the group consisting of zif 268 and TFIIIA.

32. The variant of claim 28, wherein the cellular nucleotide sequence is DNA.

33. The variant of claim 28, wherein the cellular nucleotide sequence is RNA.

34. The variant of claim 1, wherein the polypeptide contains a linker region between zinc fingers comprising the amino acid sequence TGEKP.

35. The variant of claim 28, wherein the cellular nucleotide sequence is a structural gene nucleotide sequence.

36. The variant of claim 28, wherein the cellular nucleotide sequence is a promoter nucleotide sequence.

37. The variant of claim 36, wherein the promoter is an onco-promoter.

38. The variant of claim 37, wherein the promoter is a viral promoter.

39. The variant of claim 28, wherein the cellular nucleotide sequence is a retroviral nucleotide sequence.

40. The variant of claim 39, wherein the retrovirus is a human T-cell lymphotrophic virus (HTLV).

41. The variant of claim 40, wherein the retrovirus is HTLV-1 or HTLV-2.

42. The variant of claim 39, wherein the retrovirus is a human immunodeficiency virus (HIV).

43. The variant of claim 42, wherein the retrovirus is HIV-1 or HIV-2.

44. The variant of claim 28, wherein the cellular nucleotide sequence is an oncogene nucleotide sequence.

45. The variant of claim 28, wherein the cellular nucleotide sequence is a plant cellular nucleotide sequence.

46. A zinc finger-nucleotide binding polypeptide variant produced by the method of claim 36.

47. An isolated nucleotide sequence encoding a zinc finger-nucleotide binding polypeptide variant of claim 28.

48. A recombinant expression vector containing a nucleotide sequence of claim 47.

49. A method for inhibiting a transcriptional function of a target cellular nucleotide sequence comprising a zinc finger-nucleotide binding motif, the method comprising contacting the motif with an effective amount of a zinc finger-nucleotide binding polypeptide variant comprised of at least two zinc finger molecules, wherein the amino acid sequence of each zinc finger module that binds the motif comprises two cysteines and two histidines whereby both cysteines are amino proximal to both histidines and wherein each of two modules has at least one amino acid sequence modification.

50. The method of claim 26, wherein the zinc finger binding polypeptide variant is a truncated zinc finger protein.

51. The method of claim 49, wherein the cellular nucleotide sequence is DNA.

52. The method of claim 49, wherein the cellular nucleotide sequence is RNA.

53. The method of claim 49, wherein the cellular nucleotide sequence is a structural gene nucleotide sequence.

54. The method of claim 49, wherein the cellular nucleotide sequence is a promoter nucleotide sequence.

55. The method of claim 49, wherein the cellular nucleotide sequence is an oncogene nucleotide sequence.

56. The method of claim 49, wherein the cellular nucleotide sequence is a plant cellular nucleotide sequence.

* * * * *

(FILE 'HOME' ENTERED AT 17:08:19 ON 08 FEB 2004)

FILE 'MEDLINE, EMBASE, BIOSIS, CAPLUS' ENTERED AT 17:09:06 ON 08 FEB 2004

L1	1500	S	(BARBAS, ?)/IN,AU
L2	987	S	(GOTTESFELD, ?)/IN,AU
L3	95284	S	(WRIGHT, ?)/IN,AU
L4	5	S	L1 AND L2 AND L3
L5	4		DUPLICATE REMOVE L4 (1 DUPLICATE REMOVED)
L6	97715	S	L1 OR L2 OR L3
L7	0	S	ZINC ADJ2 FINGER
L8	26640	S	ZINC (2W) FINGER
L9	276	S	L8 AND L6
L10	19	S	L9 AND ZIF268
L11	8		DUPLICATE REMOVE L10 (11 DUPLICATES REMOVED)
L12	5	S	L11 NOT L4
L13	150	S	TFIIIA AND L6
L14	4	S	L13 AND (MUTANT OR VARIANT)
L15	4	S	L14 NOT (L4 OR L10)
L16	1		DUPLICATE REMOVE L14 (3 DUPLICATES REMOVED)
L17	1416	S	L8 (S) (MUTANT OR VARIANT)
L18	431	S	L17 AND PY<1996
L19	17	S	L18 AND TFIIIA
L20	8		DUPLICATE REMOVE L19 (9 DUPLICATES REMOVED)
L21	8	S	L20 NOT (LL4 OR L10 OR L16)